

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: August 17, 2005, 11:04:38 ; Search time 160 Seconds  
 (without alignments)  
 633,880 Million cell updates/sec

**Title:** US-99-826-212A-2  
**Perfect score:** 1382  
**Sequence:** MARIKPTLKFVVVIVAVILP.....YISCTIVGIVLIVLIVLIVFV 259

**Scoring table:** BLOSUM62  
**Gapop:** 10.0 , Gapext: 0.5  
**Searched:** 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

**Database :**

Published Applications AA:  
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 22: /cgm2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep:

Pred. No.: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Length	DB.	ID	Description
1	1382	100.0	259	9	US-09-026-212-2	Sequence 2: APP
2	1382	100.0	259	9	US-09-087-879-1	Sequence 1: APP
3	1382	100.0	259	9	US-09-092-94-1	Sequence 1, APP
4	1382	100.0	259	14	US-10-028-072-00	Sequence 300,
5	1382	100.0	259	14	US-10-140-808-00	Sequence 300,
6	1382	100.0	259	14	US-10-121-049-300	Sequence 300,
7	1382	100.0	259	14	US-10-123-904-300	Sequence 300,
8	1382	100.0	259	14	US-10-140-470-00	Sequence 300,
9	1382	100.0	259	14	US-10-175-746-300	Sequence 300,
10	1382	100.0	259	14	US-10-176-913-300	Sequence 300,
11	1382	100.0	259	14	US-10-176-921-300	Sequence 300,

## SUMMARIES

US-09-826-212-2  
Sequence 2, Application US/09826212  
Patent No. US2001002116A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ying-Fei  
APPLICANT: Genz, Reiner  
APPLICANT: Ruben, Steven  
APPLICANT: Ni, Jian  
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
FILE REFERENCE: 1488-12/0006  
CURRENT APPLICATION NUMBER: US/09/826,212  
CURRENT FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2  
LENGTH: 259  
TYPE: PRT

## ALIGNMENTS

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12:	cgm2_6/ptodata/2/pubpaas/US10A				NEW	PUB.pep:**	
13:	cgm2_6/ptodata/2/pubpaas/US10B				PUBCOMB	pep:**	
14:	cgm2_6/ptodata/2/pubpaas/US10C				PUBCOMB	pep:**	
15:	cgm2_6/ptodata/2/pubpaas/US10D				PUBCOMB	pep:**	
16:	cgm2_6/ptodata/2/pubpaas/US10E				PUBCOMB	pep:**	
17:	cgm2_6/ptodata/2/pubpaas/US10F				PUBCOMB	pep:**	
18:	cgm2_6/ptodata/2/pubpaas/US10G				NEW	PUB.pep:**	
19:	cgm2_6/ptodata/2/pubpaas/US11A				PUBCOMB	pep:**	
20:	cgm2_6/ptodata/2/pubpaas/US11B				NEW	PUB.pep:**	
21:	/cgm2_6/ptodata/2/pubpaas/US60				NEW	PUB.pep:**	
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US-09-826-212-2
Sequence 2, Application US/09826212
Patent No. US2003002116A1

GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Genz, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.128006
CURRENT APPLICATION NUMBER: US/09/826.212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-212-2

Query Match          Score 1382; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.1e-85;
Matches 259; Conservative 0; Mismatches 0;

QY      1 MARIKKILKPKVNTIVAVLPLPLASATTAQEEPVQPTTARPP
QY      1 MARIKKILKPKVNTIVAVLPLPLASATTAQEEPVQPTTARPP
Db      61 RHTGAGCNPCTEGVDYTNASNNSNRPSCPCTVCKSDOKHSSC
Db      61 RHTGAGCNPCTEGVDYTNASNNSNRPSCPCTVCKSDOKHSSC
121 SPEMKRKCSGPSPGKVQVSNCISWMDIOCVSFRGANATVETI

```

GenCore version 5.1.6  
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On protein - protein search, using sw model

Run on: August 17, 2005, 10:58:37 ; Search time 23 Seconds

Title: US-09-826-212a-2  
Perfect Score: 1382  
Sequence: I. MARIPIKTLKFWVVIVAVILP.....VLSCTIVSIVIVLVLIVLVF. 259

Scoring table: BLOSUM62  
GapOpen 10.0 ; Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 51345

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

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4: /cgpn\_6/prodata/1/1aa/6B\_COMB.pep: \*  
5: /cgpn\_6/prodata/1/1aa/PCUTS\_COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

#### Result

#### No.

#### Score

#### Match Length

#### DB ID

#### Description

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3	1382	100.0	299	3	US-09-153-927-3
4	1382	100.0	299	4	US-09-134-618-4
5	1382	100.0	299	4	US-09-949-016-6422
6	1376	99.6	301	4	US-09-949-016-9189
7	634	45.9	386	3	US-09-086-4831-2
8	634	45.9	386	4	US-09-580-212-2
9	634	45.9	386	4	US-09-763-402-2
10	627	45.4	386	4	US-09-120-491-6
11	480	34.2	452	4	US-09-949-016-9855
12	472	34.2	234	4	US-09-130-491-12
13	472	34.2	467	3	US-09-086-4831-6
14	472	34.2	467	4	US-09-580-212-6
15	472	34.2	467	4	US-09-763-402-6
16	472	34.2	468	4	US-09-013-8950-2
17	472	34.2	468	4	US-09-585-918-2
18	472	34.2	468	4	US-09-448-868-2
19	472	34.2	468	4	US-09-949-016-6423
20	452	32.4	350	4	US-09-134-610-6
21	448	32.4	460	3	US-09-833-039A-2
22	448	32.4	440	4	US-09-536-201-2
23	448	32.4	440	4	US-09-578-392-2
24	398.5	28.8	424	3	US-09-323-593A-8
25	383.5	27.7	411	4	US-09-134-618-2
26	380.5	20.5	412	3	US-09-333-593A-2
27	379.5	27.5	411	3	US-09-079-029-1

#### ALIGNMENTS

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Sequence 3, Appli	30	236.5	17.1	303	3	US-09-333-593A-4
Sequence 4, Appli	31	212	15.3	368	2	US-09-051-579-2
Sequence 5, Appli	32	201.5	14.6	427	3	US-09-086-403A-4
Sequence 6, Appli	33	201.5	14.6	427	3	US-09-041-886-2
Sequence 7, Appli	34	201.5	14.6	427	3	US-09-006-353A-5
Sequence 8, Appli	35	201.5	14.6	427	4	US-09-573-986-5
Sequence 9, Appli	36	201.5	14.6	427	4	US-09-580-212-4
Sequence 10, Appli	37	201.5	14.6	427	4	US-09-769-402-4
Sequence 11, Appli	38	201.5	14.6	427	4	US-09-748-537-13
Sequence 12, Appli	39	201.5	14.6	427	4	US-10-092-138A-24
Sequence 13, Appli	40	201.5	14.6	427	4	US-09-949-016-6233
Sequence 14, Appli	41	201.5	14.6	455	3	US-09-527-036A-4
Sequence 15, Appli	42	201.5	14.6	455	4	US-09-756-054-4
Sequence 16, Appli	43	201.5	14.6	464	4	US-09-949-016-9441
Sequence 17, Appli	44	201.5	14.5	425	4	US-09-748-537-14
Sequence 18, Appli	45	198	14.3	398	4	US-09-612-033B-14

RESULT 1					
US-09-006-353A-2					
Sequence 1, Application US/09006353A					
; Patent No. 6261801					
GENERAL INFORMATION:					
APPLICANT: HEI, YING-FEI					
APPLICANT: YU, GUO-LIANG					
APPLICANT: GENTZ, REINER					
APPLICANT: ROBIN, STEVEN					
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5					
NUMBER OF SEQURENCES: 26					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: HUMAN GENOME SCIENCES, INC.					
STREET: 9410 KEY WEST AVENUE					
CITY: ROCKVILLE					
STATE: MD					
COUNTRY: US					
ZIP: 20850					
COMPUTER READABLE FORM:					
MEDIUM TYPE: Floppy disk					
COMPUTER: IBM PC compatible					
OPERATING SYSTEM: PC-DOS/MS-DOS					
CURRENT APPLICATION DATA: US/09-006-353A					
APPLICATION NUMBER: US/09-006-353A					
FILING DATE: 2004-01-06					
CLASSIFICATION: 435					
ATTORNEY/AGENT INFORMATION:					
NAME: BROOKES, ANDERS A					
REGISTRATION NUMBER: 36,373					
REFERENCE DOCKET NUMBER: PFP341					
TELECOMMUNICATION INFORMATION:					
TELEPHONE: (301) 309-8512					
TELEX/FAX: (301) 309-8512					
INFORMATION FOR SEQ ID NO: 2:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 259 amino acids					
TYPE: amino acid					
TOPOLOGY: linear					
MOLECULAR TYPE: protein					
US-09-006-353A-2					
Query Match Best Local Similarity 100.0%; Pred. No. 1.4e-101; Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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Db 1 MARIPIKTLKFWVVIVAVILP.....VLSCTIVSIVIVLVLIVLVF. 259					
Sequence 2, Appli					
Sequence 3, Appli					
Sequence 4, Appli					
Sequence 5, Appli					
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## OM nucleic - nucleic search, using SW mode!

Run on: August 19, 2005, 06:54:16 ; Search time: 988 Seconds  
(without alignments)

9153.554 Million cell updates/sec

## Title:

US-09-826-212a-1

## Perfect score:

1392

## Sequence:

1. cctccacgcccggcact.....agatttccgtaaaaaa 1392

## Scoring table:

IDENTITY\_NUC

## Gapop:

10.0 , Gapext: 1.0

## Searched:

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## Total number of hits satisfying chosen parameters:

14632570

## Minimum DB seq length:

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## Maximum DB seq length:

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## Post-processing:

Minimum Match 0%

## Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1392	100.0	1392	9 US-09-826-212-1 Sequence 1, Appli
2	1392	100.0	1392	15 US-10-186-643-1 Sequence 1, Appli
3	1311.6	94.2	1365	21 US-10-485-233-1 Sequence 1, Appli
4	1103	79.2	1180	9 US-09-887-879-2 Sequence 4, Appli
5	1103	79.2	1180	9 US-09-887-879-4 Sequence 2, Appli
6	1103	79.2	1180	9 US-09-992-964-2 Sequence 4, Appli
7	1103	79.2	1180	9 US-09-992-964-4 Sequence 2, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

## RESULT 1

US-09-826-212-1

Sequence 1, Application US/09826212

; Patent No. US20010021516A1

; GENERAL INFORMATION:

; APPLICANT: Wei, Ying-Fei

; APPLICANT: Genitz, Reiner

; APPLICANT: Ruben, Steven

; APPLICANT: Ni, Jian

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

; FILE REFERENCE: 1488.128006

; CURRENT APPLICATION NUMBER: US/09-826, 212

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 1

; LENGTH: 1392

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: CDS

; NAME/KEY: CDS

; LOCATION: (183)..(959)

; NAME/KEY: mact-peptide

; LOCATION: (261)..()

; NAME/KEY: s1g-peptide

; LOCATION: (183)..(260)

; US-09-826-212-1

; Query Match Similarity 100.0%; Score 1392; DB 9; Length 1392;

; Best Local Similarity 100.0%; Pred. No. 0;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic -- nucleic search, using sw model.  
Run on: August 19, 2005, 04:06:21 ; Search time 264 Seconds  
(without alignments)

Title: US-09-826-212a-1  
Perfect score: 1392  
Sequence: 1 ccttcacgacgtttccgtaaaaaa 1392  
8627.641 Million cell updates/sec.

scoring table: IDENTITY\_NUC  
Gapop 10-0 Gapext 1.0  
Searched: 1202784 seqs, 818138359 residues  
Total number of hits satisfying chosen parameters: 2405568  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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5: /cgn2\_6/prodata/1/ina/PCTUS.COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

RESULT 1  
US-09-006-353A-1

Sequence 1, Application US/09006353A

Patent No. 6261801

## GENERAL INFORMATION:

APPLICANT: WEI, YING-PEI

APPLICANT: YU, GUO-LIANG

APPLICANT: GEMZY, REINER

APPLICANT: RUBEN, STEVEN

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: HUMAN GENOME SCIENCES, INC.

SUBJECT: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISKCOMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A

REGISTRATION NUMBER: 36-373

REFERENCE/DOCKET NUMBER: FB341

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1392 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE: NAME/KEY: CDS

LOCATION: 183..959

FEATURE: NAME/KEY: big\_peptide

LOCATION: 183..260

FEATURE: NAME/KEY: mat\_peptide

LOCATION: 261..959